

re-run #11

RAW SEQUENCE LISTING

DATE: 01/08/2002

PATENT APPLICATION: US/09/759,595

TIME: 10:53:49

Input Set : A:\-39-1.app

Output Set: N:\CRF3\01082002\I759595.raw

ENTERED

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3 <110> APPLICANT: Wesche, Holger
4     Li, Shyun
5     Tularik Inc.
7 <120> TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
9 <130> FILE REFERENCE: 018781-003910US
11 <140> CURRENT APPLICATION NUMBER: US 09/759,595
12 <141> CURRENT FILING DATE: 2001-01-11
14 <150> PRIOR APPLICATION NUMBER: US 60/176,395
15 <151> PRIOR FILING DATE: 2000-01-13
17 <160> NUMBER OF SEQ ID NOS: 7
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 460
23 <212> TYPE: PRT
24 <213> ORGANISM: Homo sapiens
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31             20             25             30
33 Lys Lys Leu Ala Val Ala Ile Lys Lys Pro Ser Gly Asp Asp Arg Tyr
34             35             40             45
36 Asn Gln Phe His Ile Arg Arg Phe Glu Ala Leu Leu Gln Thr Gly Lys
37             50             55             60
39 Ser Pro Thr Ser Glu Leu Leu Phe Asp Trp Gly Thr Thr Asn Cys Thr
40             65             70             75             80
42 Ala Gly Asp Leu Val Asp Leu Leu Ile Gln Asn Glu Phe Phe Ala Pro
43             85             90             95
45 Ala Ser Leu Leu Leu Pro Asp Ala Val Pro Lys Thr Ala Asn Thr Leu
46             100            105            110
48 Pro Ser Lys Glu Ala Ile Thr Val Gln Gln Lys Gln Met Pro Phe Cys
49             115            120            125
51 Asp Lys Asp Arg Thr Leu Met Thr Pro Val Gln Asn Leu Glu Gln Ser
52             130            135            140
54 Tyr Met Pro Pro Asp Ser Ser Ser Pro Glu Asn Lys Ser Leu Glu Val
55             145            150            155            160
57 Ser Asp Thr Arg Phe His Ser Phe Ser Phe Tyr Glu Leu Lys Asn Val
58             165            170            175
60 Thr Asn Asn Phe Asp Glu Arg Pro Ile Ser Val Gly Gly Asn Lys Met
61             180            185            190
63 Gly Glu Gly Gly Phe Gly Val Val Tyr Lys Gly Tyr Val Asn Asn Thr
64             195            200            205
66 Thr Val Ala Val Lys Lys Leu Ala Ala Met Val Asp Ile Thr Thr Glu
67             210            215            220
69 Glu Leu Lys Gln Gln Phe Asp Gln Glu Ile Lys Val Met Ala Lys Cys
70             225            230            235            240
72 Gln His Glu Asn Leu Val Glu Leu Leu Gly Phe Ser Ser Asp Gly Asp

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73          245          250          255
75 Asp Leu Cys Leu Val Tyr Val Tyr Met Pro Asn Gly Ser Leu Leu Asp
76          260          265          270
78 Arg Leu Ser Cys Leu Asp Gly Thr Pro Pro Leu Ser Trp His Met Arg
79          275          280          285
81 Cys Lys Ile Ala Gln Gly Ala Ala Asn Gly Ile Asn Phe Leu His Glu
82          290          295          300
84 Asn His His Ile His Arg Asp Ile Lys Ser Ala Asn Ile Leu Leu Asp
85 305          310          315          320
87 Glu Ala Phe Thr Ala Lys Ile Ser Asp Phe Gly Leu Ala Arg Ala Ser
88          325          330          335
90 Glu Lys Phe Ala Gln Thr Val Met Thr Ser Arg Ile Val Gly Thr Thr
91          340          345          350
93 Ala Tyr Met Ala Pro Glu Ala Leu Arg Gly Glu Ile Thr Pro Lys Ser
94          355          360          365
96 Asp Ile Tyr Ser Phe Gly Val Val Leu Leu Glu Ile Ile Thr Gly Leu
97          370          375          380
99 Pro Ala Val Asp Glu His Arg Glu Pro Gln Leu Leu Leu Asp Ile Lys
100 385          390          395          400
102 Glu Glu Ile Glu Asp Glu Glu Lys Thr Ile Glu Asp Tyr Ile Asp Lys
103          405          410          415
105 Lys Met Asn Asp Ala Asp Ser Thr Ser Val Glu Ala Met Tyr Ser Val
106          420          425          430
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121 <223> OTHER INFORMATION: human IL-1 receptor-associated kinase 4 (IRAK-4)
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124 <220> FEATURE:
125 <221> NAME/KEY: CDS
126 <222> LOCATION: (1)..(1383)
127 <223> OTHER INFORMATION: human IRAK-4
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132 aaaccatctg gtgatgatag atacaatcag tttcacataa ggagatttga agcattactt 180
133 caaactggaa aaagtcccac ttctgaatta ctgtttgact ggggcaccac aaattgcaca 240
134 gctggtgatc ttgtggatct tttgatccaa aatgaatttt ttgctcctgc gagtcttttg 300
135 ctcccagatg ctgttcccaa aactgctaata acactacctt ctaaagaagc tataacagtt 360
136 cagcaaaaaac agatgccttt ctgtgacaaa gacaggacat tgatgacacc tgtgcagaat 420
137 cttgaacaaa gctatatgcc acctgactcc tcaagtccag aaaataaaaag tttagaagtt 480
138 agtgatacac gttttcacag tttttcattt tatgaattga agaatgtcac aaataacttt 540
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140 tataaaggct acgtaaataa cacaactgtg gcagtgaaga agcttgcagc aatgggttgac 660
141 attactactg aagaactgaa acagcagttt gatcaagaaa taaaagtaat ggcaaagtgt 720
142 caacatgaaa acttagtaga actacttggg ttctcaagtg atggagatga cctctgctta 780
143 gtatatgttt acatgcctaa tggttcattg ctagacagac tctcttgcct ggatgggtact 840
144 ccaccacttt cttggcacat gagatgcaag attgctcagg gtgcagctaa tggcatcaat 900
145 tttctacatg aaaatcatca tattcataga gatattaaaa gtgcaaatat cttactggat 960
146 gaagctttta ctgctaaaat atctgacttt ggccttgcac gggcttctga gaagtttgcc 1020
147 cagacagtca tgactagcag aattgtggga acaacagctt atatggcacc agaagctttg 1080
148 cgtggagaaa taacacccaa atctgatatt tacagctttg gtgtgggttt actagaaata 1140
149 ataactggac ttccagctgt ggatgaacac cgtgaacctc agttattgct agatattaaa 1200
150 gaagaaattg aagatgaaga aaagacaatt gaagattata ttgataaaaa gatgaatgat 1260
151 gctgattcca cttcagttga agctatgtac tctgttgcta gtcaatgtct gcatgaaaag 1320
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153 taa 1383

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156 <210> SEQ ID NO: 3

157 <211> LENGTH: 459

158 <212> TYPE: PRT

159 <213> ORGANISM: Mus sp.

161 <400> SEQUENCE: 3

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165 Gly Ile Leu Arg Lys Leu Ser Asp Phe Ile Asp Pro Gln Glu Gly Trp
166           20           25           30
168 Lys Lys Leu Ala Val Ala Ile Lys Lys Pro Ser Gly Asp Asp Arg Tyr
169           35           40           45
171 Asn Gln Phe His Ile Arg Arg Phe Glu Ala Leu Leu Gln Thr Gly Lys
172           50           55           60
174 Ser Pro Thr Cys Glu Leu Leu Phe Asp Trp Gly Thr Thr Asn Cys Thr
175   65           70           75           80
177 Val Gly Asp Leu Val Asp Leu Leu Val Gln Ile Glu Leu Phe Ala Pro
178           85           90           95
180 Ala Thr Leu Leu Leu Pro Asp Ala Val Pro Gln Thr Val Lys Ser Leu
181           100          105          110
183 Pro Pro Arg Glu Ala Ala Thr Val Ala Gln Thr His Gly Pro Cys Gln
184           115          120          125
186 Glu Lys Asp Arg Thr Ser Val Met Pro Met Pro Lys Leu Glu His Ser
187           130          135          140
189 Cys Glu Pro Pro Asp Ser Ser Ser Pro Asp Asn Arg Ser Val Glu Ser
190   145          150          155          160
192 Ser Asp Thr Arg Phe His Ser Phe Ser Phe His Glu Leu Lys Ser Ile
193           165          170          175
195 Thr Asn Asn Phe Asp Glu Gln Pro Ala Ser Ala Gly Gly Asn Arg Met
196           180          185          190
198 Gly Glu Gly Gly Phe Gly Val Val Tyr Lys Gly Cys Val Asn Asn Thr
199           195          200          205
201 Ile Val Ala Val Lys Lys Leu Gly Ala Met Val Glu Ile Ser Thr Glu
202           210          215          220
204 Glu Leu Lys Gln Gln Phe Asp Gln Glu Ile Lys Val Met Ala Thr Cys
205   225          230          235          240

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207 Gln His Glu Asn Leu Val Glu Leu Leu Gly Phe Ser Ser Asp Ser Asp
208                               245                               250                               255
210 Asn Leu Cys Leu Val Tyr Ala Tyr Met Pro Asn Gly Ser Leu Leu Asp
211                               260                               265                               270
213 Arg Leu Ser Cys Leu Asp Gly Thr Pro Pro Leu Ser Trp His Thr Arg
214                               275                               280                               285
216 Cys Lys Val Ala Gln Gly Thr Ala Asn Gly Ile Arg Phe Leu His Glu
217                               290                               295                               300
219 Asn His His Ile His Arg Asp Ile Lys Ser Ala Asn Ile Leu Leu Asp
220 305                               310                               315                               320
222 Lys Asp Phe Thr Ala Lys Ile Ser Asp Phe Gly Leu Ala Arg Ala Ser
223                               325                               330                               335
225 Ala Arg Leu Ala Gln Thr Val Met Thr Ser Arg Ile Val Gly Thr Thr
226                               340                               345                               350
228 Ala Tyr Met Ala Pro Glu Ala Leu Arg Gly Glu Ile Thr Pro Lys Ser
229                               355                               360                               365
231 Asp Ile Tyr Ser Phe Gly Val Val Leu Leu Glu Leu Ile Thr Gly Leu
232                               370                               375                               380
234 Ala Ala Val Asp Glu Asn Arg Glu Pro Gln Leu Leu Leu Asp Ile Lys
235 385                               390                               395                               400
237 Glu Glu Ile Glu Asp Glu Glu Lys Thr Ile Glu Asp Tyr Thr Asp Glu
238                               405                               410                               415
240 Lys Met Ser Asp Ala Asp Pro Ala Ser Val Glu Ala Met Tyr Ser Ala
241                               420                               425                               430
243 Ala Ser Gln Cys Leu His Glu Lys Lys Asn Arg Arg Pro Asp Ile Ala
244                               435                               440                               445
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251 <211> LENGTH: 1542
252 <212> TYPE: DNA
253 <213> ORGANISM: Mus sp.
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256 <223> OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4)
257      cDNA
259 <220> FEATURE:
260 <221> NAME/KEY: CDS
261 <222> LOCATION: (163)..(1542)
262 <223> OTHER INFORMATION: murine IRAK-4
264 <400> SEQUENCE: 4
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267 gccttgcca ggaagcgagg gacgtccgag aggaagtaga agatgaacaa gccgttgaca 180
268 ccatcgacat acatacgcaa ccttaattgtg gggatcctta ggaagctgtc ggattttatt 240
269 gatcctcaag aaggggtggaa gaaattagca gtagctatca aaaagccgtc cggcgacgac 300
270 agataacaatc agttccatat aaggagattc gaagccttac ttcagaccgg gaagagcccc 360
271 acctgtgaac tgctgtttga ctggggcacc acgaactgca cagttggcga ccttggtgat 420
272 ctactgggtc agattgagct gtttgcccc gccactctcc tgctgccgga tgccgttccc 480
273 caaaccgtca aaagcctgcc tcctagagaa gcggcaacag tggcacaaac acacggggcct 540

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274 tgtcaggaaa aggacaggac atccgtaatg cctatgccga agctagaaca cagctgcgag 600
275 ccaccggact cctcaagccc agacaacaga agtgtagagt ccagcgacac tcggttccac 660
276 agcttctcgt tccatgaact gaagagcatc acaaacaact tcgacgagca acccgcgctt 720
277 gccggtggca accggatggg agagggggga tttggagtgg tgtacaaggg ctgtgtgaac 780
278 aacaccatcg tggcggtgaa gaagctcgga gcgatggttg aaatcagtac tgaagaacta 840
279 aagcaacagt ttgatcaaga aattaaagta atggcaacgt gtcagcacga gaacctggtg 900
280 gagctgctcg gcttctccag cgacagcgac aacctgtgct tagtgtatgc ttacatgccc 960
281 aacgggtcct tgctggacag actgtcctgc ctggatggta caccaccgct ttcttggcac 1020
282 acaaggtgca aggttgctca ggggacagca aatggcatca ggtttctgca tgaaaatcat 1080
283 cacattcata gagatattaa aagtgc aaat atcttactag acaaagactt tactgccaaa 1140
284 atatctgact ttgggcttgc acgggcttcg gcaaggctag cgcagacggt catgaccagc 1200
285 cgaatcgtgg gcacaacggc ttacatggca cccgaagctt tgcggggaga aataacaccc 1260
286 aaatctgaca tctacagctt cggcgtggtt ctgttggagc tgataaccgg gctggcggct 1320
287 gtggatgaaa accgtgaacc tcaactactg ctggatatta aagaagagat tgaagatgaa 1380
288 gagaagacga ttgaagatta cacggatgag aagatgagcg atgcggaccc tgcttcggtg 1440
289 gaagcaatgt actctgctgc tagccagtgt ctgcatgaga agaaaaacag acggccagac 1500
290 attgcaaagg ttcaacagct gctacaagag atgtctgctt aa 1542
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294 <211> LENGTH: 34
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial Sequence
298 <220> FEATURE:
299 <223> OTHER INFORMATION: Description of Artificial Sequence:sense primer
300 for amplification of human IRAK-4
302 <400> SEQUENCE: 5
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306 <210> SEQ ID NO: 6
307 <211> LENGTH: 25
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
312 <223> OTHER INFORMATION: Description of Artificial Sequence:antisense
313 primer for amplification of human IRAK-4
315 <400> SEQUENCE: 6
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319 <210> SEQ ID NO: 7
320 <211> LENGTH: 8
321 <212> TYPE: PRT
322 <213> ORGANISM: Artificial Sequence
324 <220> FEATURE:
325 <223> OTHER INFORMATION: Description of Artificial Sequence:epitope tag
327 <400> SEQUENCE: 7
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VERIFICATION SUMMARY

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Input Set : A:\-39-1.app

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